(b) extending the primers to form complementary primer extension products which act as templates for synthesizing the desired DNA fragment containing the repeat region;

(c) detecting the fragment so amplified; and

(d) analyzing the amplified DNA fragment for [a repeat region comprising a CTG repeat] an at-risk allele having at least about 80 CTG repeats in the repeat region or at least about 92 combined CTA and CTG repeats in the repeat region.

2. The method of claim 1 wherein a first oligonucleotide primer of the two oligonucleotide primers is chosen from nucleotides 1-448 of SEQ ID NO:1, and a second oligonucleotide primer of the two oligonucleotide primers is chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, wherein each primer has at least 11 nucleotides.

3. The method of claim 2 wherein the first oligonucleotide primer is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:8, and SEQ ID NO:4 and wherein the second oligonucleotide primer is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, and SEQ ID NO:12.

43 (**Amended**) A kit for detecting whether or not an individual has, or is at-risk for developing, spinocerebellar ataxia type 8, the kit comprising a first oligonucleotide primer chosen from nucleotides 1-448 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, wherein each primer has at least 11 nucleotides, wherein an individual who has or is at risk for developing SCA8 has an at-risk allele having at least about 80 CTG repeats in the repeat region or at least about 92 combined CTA and CTG repeats in the repeat region.

5. (**Canceled**)

6. **(Canceled)**

7. A method for detecting the presence of at least one DNA molecule containing a repeat region of an SCA8 coding sequence comprising:

(a) digesting genomic DNA with a restriction endonuclease to obtain DNA fragments;

(b) denaturating the DNA fragments to yield DNA molecules and probing the DNA molecules under hybridizing conditions with a detectably labeled probe, which hybridizes to a DNA molecule containing a repeat region of an isolated SCA8 coding sequence;

(c) detecting the probe which has hybridized to the DNA molecule; and

(d) analyzing the DNA molecule for a repeat region characteristic of a normal or at-risk form of the SCA8 coding sequence.

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8. The method of claim 7 wherein the probe is chosen from nucleotides 1-448 of SEQ ID NO:1 or from nucleotides 726-1,159 of SEQ ID NO:1, or complements thereto, wherein the probe has at least 20 nucleotides.

9.. The method of claim 7 wherein the probe comprises nucleotides 19-449 of SEQ ID NO:1, or a complement thereto.

10. (**Amended**) A kit for detecting whether or not an individual has, or is at-risk for developing, spinocerebellar ataxia type 8 comprising a probe chosen from nucleotides 1-448 of SEQ ID NO:1 or from nucleotides 726-1,159 of SEQ ID NO:1, or complements thereto, wherein each probe has at least 20 nucleotides, wherein an individual who has or is at risk for developing SCA8 has an at-risk allele having at least about 80 CTG repeats in the repeat region or at least about 92 combined CTA and CTG repeats in the repeat region.

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11. (**Amended**) The method of claim 7 wherein the step of analyzing comprises analyzing for a repeat region comprising [a $(CTG)_n$ repeat wherein n is] at least about 80 CTG repeats.

12. (**Amended**) The method of claim 7 wherein the step of analyzing comprises analyzing for a repeat region comprising [a combined $((CTG)/(CTA))_n$ repeat wherein n is] at least about 92 combined CTA and CTG repeats.

13. (**Amended**) A method for determining whether an individual [has, or] is not at-risk for developing, spinocerebellar ataxia type 8, the method comprising analyzing a repeat region of a spinocerebellar ataxia type 8 coding sequence wherein individuals who are not at-risk for developing spinocerebellar ataxia type 8 have less than 80 CTG repeats in the repeat region or no greater than about 91 combined CTA and CTG repeats in the repeat region.

14. (**Amended**) A method for detecting the presence of a DNA fragment located within an at-risk allele of the SCA8 coding sequence comprising:

(a) treating separate complementary DNA molecules of a DNA fragment containing a repeat region of the SCA8 coding sequence with a molar excess of a first oligonucleotide primer pair;

(b) extending the first primer pair to form complementary primer extension products which act as templates for synthesizing a first desired DNA fragment containing the repeat region;

(c) removing the first desired DNA fragment containing the repeat region;

(d) treating separate complementary strands of the first desired DNA fragment containing the repeat region with a molar excess of a second oligonucleotide primer pair;

(e) extending the second primer pair to form complementary primer extension products which act as templates for synthesizing a second desired DNA fragment containing the repeat region;

(f) detecting the second desired DNA fragment so amplified; and

(g) analyzing the amplified DNA fragment for [a repeat region] an at-risk allele having at least about 80 CTG repeats in the repeat region or at least about 92 combined CTA and CTG repeats in the repeat region.

15. The method of claim 14 wherein the first oligonucleotide primer pair comprises a first oligonucleotide primer chosen from nucleotides 1-448 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, wherein each primer has at least 11 nucleotides.

16. The method of claim 15 wherein the first oligonucleotide primer is selected from the group consisting of SEQ ID NO:5, SEQ ID NO:8, and SEQ ID NO:4 and wherein the second oligonucleotide primer is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:9, and SEQ ID NO:12.

17. The method of claim 14 wherein the second oligonucleotide primer pair comprises a first oligonucleotide primer chosen from nucleotides 449-725 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, wherein each primer has at least 11 nucleotides.

18. (**Amended**) A kit for detecting whether or not an individual has, or is at-risk for, developing spinocerebellar ataxia type 8 comprising a first oligonucleotide primer pair comprising a first oligonucleotide primer chosen from nucleotides 1-448 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, and a second oligonucleotide primer pair comprising a first oligonucleotide primer chosen from nucleotides 449-725 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, wherein each primer has at least 11 nucleotides.

wherein an individual who has or is at risk for developing SCA8 has an at-risk allele having at least about 80 CTG repeats in the repeat region or at least about 92 combined CTA and CTG repeats in the repeat region.

19. The method of claim 14 wherein the second oligonucleotide primer pair comprises a first oligonucleotide primer that has three CTA repeats followed by three CTG repeats and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1.

20. **(Canceled)**

21. (**Amended**) An isolated SCA8 coding sequence [nucleic acid molecule] comprising [containing] a repeat region wherein the SCA8 locus is located on the long arm of chromosome 13 [of an isolated spinocerebellar ataxia type 8 (SCA8) coding sequence, the coding sequence located within the long arm of chromosome 13], and a complement of the coding sequence [nucleic acid molecule].

22. (**Amended**) ~~The isolated coding sequence~~ [nucleic acid molecule] of claim 21 wherein the nucleic acid comprises DNA.

23. The DNA of claim 22 wherein the DNA is cDNA.

24. The DNA of claim 22 wherein the cDNA comprises SEQ ID NO:2.

25. The DNA of claim 22 wherein the cDNA comprises SEQ ID NO:3.

26. (**Amended**) ~~The~~ isolated coding sequence [nucleic acid molecule] of claim 21 wherein the nucleic acid comprises SEQ ID NO:1.

27. An isolated nucleic acid molecule wherein the nucleic acid comprises 1-448 of SEQ ID NO:1, and a complement thereto.

28. An isolated nucleic acid molecule wherein the nucleic acid comprises 726-1,159 of SEQ ID NO:1, and a complement thereto.

29. (**Amended**) The isolated coding sequence [nucleic acid molecule] of claim 21 wherein the SCA8 coding sequence comprises nucleotides 1-448 of SEQ ID NO:1 followed by a repeat region.

30. (**Amended**) The isolated coding sequence [nucleic acid molecule] of claim 21 wherein the SCA8 coding sequence comprises nucleotides 726-1,159 of SEQ ID NO:1 preceded by a repeat region.

31. An isolated nucleic acid molecule comprising nucleotides 1-448 of SEQ ID NO:1 in a vector.

32. An isolated nucleic acid molecule comprising nucleotides 1-448 of SEQ ID NO:1 and further comprising a repeat region, and a complement thereto.

33. An isolated oligonucleotide comprising at least 15 nucleotides from nucleotides 1-448 of SEQ ID NO:1, and the complementary nucleotides thereto.

34. An isolated oligonucleotide comprising at least 15 nucleotides from nucleotides 726-1,159 of SEQ ID NO:1, and the complementary nucleotides thereto.

35. (**Amended**) An isolated oligonucleotide that hybridizes to a nucleic acid molecule comprising [containing] a repeat region of an isolated SCA8 coding sequence, wherein

the oligonucleotide hybridizes ~~to the SCA8 coding sequence of the long arm of~~ chromosome 13; the oligonucleotide having at least about 11 nucleotides.

36. An isolated recombinant vector comprising the nucleotides of SEQ ID NO:1 operatively linked to heterologous vector sequences.

Please add the following new claims:

37. (**New**) The method of claim ~~13~~ 16 wherein individuals who are not at-risk for developing spinocerebellar ataxia type 8 have no greater than about 33 combined CTA and CTG repeats in the repeat region.

38. (**New**) A method for detecting the presence of a DNA fragment located within a not at-risk allele of the SCA8 coding sequence comprising:

(a) treating separate complementary DNA molecules of a DNA fragment containing a repeat region of the SCA8 coding sequence with a molar excess of two oligonucleotide primers;

(b) extending the primers to form complementary primer extension products which act as templates for synthesizing the desired DNA fragment containing the repeat region;

(c) detecting the fragment so amplified; and

(d) analyzing the amplified DNA fragment for a not at-risk allele having less than 80 CTG repeats in the repeat region or no greater than about 91 combined CTA and CTG repeats in the repeat region.

39. (**New**) A method for detecting the presence of a DNA fragment located within a not at-risk allele of the SCA8 coding sequence comprising:

(a) treating separate complementary DNA molecules of a DNA fragment containing a repeat region of the SCA8 coding sequence with a molar excess of a first

oligonucleotide primer pair;

(b) extending the first primer pair to form complementary primer extension products which act as templates for synthesizing a first desired DNA fragment containing the repeat region;

(c) removing the first desired DNA fragment containing the repeat region;

(d) treating separate complementary strands of the first desired DNA fragment containing the repeat region with a molar excess of a second oligonucleotide primer pair;

(e) extending the second primer pair to form complementary primer extension products which act as templates for synthesizing a second desired DNA fragment containing the repeat region;

(f) detecting the second desired DNA fragment so amplified; and

(g) analyzing the amplified DNA fragment for a not at-risk allele having less than 80 CTG repeats in the repeat region or no greater than about 91 combined CTA and CTG repeats in the repeat region.

40. (**New**) A method for determining whether an individual has, or is at-risk for developing, spinocerebellar ataxia type 8, the method comprising analyzing a repeat region of a spinocerebellar ataxia type 8 coding sequence wherein individuals who are at-risk for developing spinocerebellar ataxia type 8 have at least about 80 CTG repeats in the repeat region or at least about 92 combined CTA and CTG repeats in the repeat region.

41. (**New**) An isolated nucleic acid molecule wherein a complement ~~of the~~ nucleic acid molecule hybridizes to nucleotides ~~1-448 of~~ SEQ ID NO:1 under standard hybridization conditions.

42. (**New**) ~~An isolated~~ nucleic acid molecule wherein a complement of the nucleic acid molecule hybridizes to nucleotides ~~726-1,159 of SEQ~~ ID NO:1 under standard

hybridization conditions.

43.16 (**New**) A kit for detecting whether or not an individual is not at-risk for developing spinocerebellar ataxia type 8, the kit comprising a first oligonucleotide primer chosen from nucleotides 1-448 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, wherein each primer has at least 11 nucleotides, wherein an individual who is not at risk for developing SCA8 has a not at-risk allele having less than 80 CTG repeats in the repeat region or no greater than about 91 combined CTA and CTG repeats in the repeat region.

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44.17 (**New**) The kit of claim 43 (16) wherein the number of combined CTA and CTG repeats in the repeat region is no greater than about 33.

45.18 (**New**) A kit for detecting whether or not an individual is not at-risk for developing spinocerebellar ataxia type 8 comprising a probe chosen from nucleotides 1-448 of SEQ ID NO:1 or from nucleotides 726-1,159 of SEQ ID NO:1, or complements thereto, wherein each probe has at least 20 nucleotides, wherein an individual who is not at risk for developing SCA8 has a not at-risk allele having less than 80 CTG repeats in the repeat region or no greater than about 91 combined CTA and CTG repeats in the repeat region.

46.19 (**New**) The kit of claim 45 (18) wherein the number of combined CTA and CTG repeats in the repeat region is no greater than about 33.

47.20 (**New**) A kit for detecting whether or not an individual is not at-risk for developing spinocerebellar ataxia type 8 comprising a first oligonucleotide primer pair comprising a first oligonucleotide primer chosen from nucleotides 1-448 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides

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726-1,159 of SEQ ID NO:1, and a second oligonucleotide primer pair comprising a first oligonucleotide primer chosen from nucleotides 449-725 of SEQ ID NO:1, and a second oligonucleotide primer chosen from nucleotides complementary to nucleotides 726-1,159 of SEQ ID NO:1, wherein each primer has at least 11 nucleotides, wherein an individual who is not at risk for developing SCA8 has a not at-risk allele having less than 80 CTG repeats in the repeat region or no greater than about 91 combined CTA and CTG repeats in the repeat region.

48. (**New**) The kit of claim 20 wherein the number of combined CTA and CTG repeats in the repeat region is no greater than about 33.

49. (**New**) The method of claim 13 wherein the analyzing comprises sequencing the repeat region of the spinocerebellar ataxia type 8 coding sequence.

50. (**New**) The method of claim 21 wherein the nucleic acid molecule is RNA.

51. (**New**) The method of claim 7 wherein the analyzing comprises detecting the length of the repeat region.

Remarks

Claims 5, 6, and 20 having been canceled, claims 1, 4, 10-14, 18, 21-22, 26, 29-30, and 35 having been amended, and claims 37-51 having been added, claims 1-4, 7-19, and 21-51 are pending.

The specification has been amended at page 35 to correct a grammatical error.

The amendment to claim 1 is supported by, for instance, originally filed claims 5 and 6.

The amendment to claims 4, 10, 14, and 18 is supported by the specification at, for instance, page 13, lines 14-25.

The amendment to claims 11 and 12 is made to clarify the scope of the claims.